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- 1 Calisher CH, Carroll D, Colwell R, et al. Science, not speculation, is essential to determine how SARS-CoV-2 reached humans. Lancet 2021; 398: 209-11.
- Calisher C, Carroll D, Colwell R, et al. Statement in support of the scientists, public health professionals, and medical professionals of China combatting COVID-19. Lancet 2020; 395: e42-43.
- Thacker PD. The COVID-19 lab leak hypothesis: did the media fall victim to a misinformation campaign? BMJ 2021; 374: n1656.
- 4 Andersen KG, Rambaut A, Lipkin WI, Holmes EC, Garry RF. The proximal origin of SARS-CoV-2. Nat Med 2020; **26:** 450–52.
- 5 Sallard E, Halloy J, Casane D, Decroly E, van Helden J. Tracing the origins of SARS-COV-2 in coronavirus phylogenies: a review. Environ Chem Lett 2021; published online Feb 4. https://dx.doi.org/10.1007%2 F510311-020-01151-1.
- 6 Yount B, Curtis KM, Fritz EA, et al. Reverse genetics with a full-length infectious cDNA of severe acute respiratory syndrome coronavirus. Proc Natl Acad Sci USA 2003; 100: 12995–3000.
- 7 Cockrell AS, Beall A, Yount B, Baric R. Efficient reverse genetic systems for rapid genetic manipulation of emergent and preemergent infectious coronaviruses. In: Perez DR, ed. Reverse genetics of RNA viruses. New York, NY: Springer New York, 2017: 59–81.
- 8 Zhou P, Yang X-L, Wang X-G, et al. A pneumonia outbreak associated with a new coronavirus of probable bat origin. *Nature* 2020; 579: 270–73.
- 9 Choo SW, Zhou J, Tian X, et al. Are pangolins scapegoats of the COVID-19 outbreak-CoV transmission and pathology evidence? Conserv Lett 2020; 13: e12754.
- 10 Frutos R, Serra-Cobo J, Chen T, Devaux CA. COVID-19: time to exonerate the pangolin from the transmission of SARS-CoV-2 to humans. Infect Genet Evol 2020; 84: 104493
- 11 Lee J, Hughes T, Lee M-H, et al. No evidence of coronaviruses or other potentially zoonotic viruses in Sunda pangolins (Manis javanica) entering the wildlife trade via Malaysia. EcoHealth 2020; published online Nov 23. https://doi.org/10.1007/s10393-020-01503-x.

- 12 WHO. WHO-convened global study of the origins of SARS-CoV-2: terms of references for the China part. World Health Organisation: Geneva, Switzerland, 2020. https://www.who.int/publications/m/item/who-convened-global-study-of-the-origins-of-sars-cov-2 (accessed Sept 14, 2021).
- 13 Joint WHO-China Study Team. WHO-convened global study of origins of SARS-CoV-2: China part. World Health Organisation: Geneva, Switzerland, 2021.
- 14 WHO. WHO calls for further studies, data on origin of SARS-CoV-2 virus, reiterates that all hypotheses remain open. https://www.who.int/news/item/30-03-2021-who-calls-for-further-studies-data-on-origin-of-sars-cov-2-virus-reiterates-that-all-hypotheses-remain-open (accessed Sept 5, 2021).
- 15 Segreto R, Deigin Y. The genetic structure of SARS-CoV-2 does not rule out a laboratory origin: SARS-COV-2 chimeric structure and furin cleavage site might be the result of genetic manipulation. BioEssays 2020; 43: e2000240.
- Deigin Y, Segreto R. SARS-CoV-2's claimed natural origin is undermined by issues with genome sequences of its relative strains: coronavirus sequences RaTG13, MP789 and RmYN02 raise multiple questions to be critically addressed by the scientific community. BioEssays 2021; 43: 2100015.
- 17 Menachery VD, Yount BL, Debbink K, et al. A SARS-like cluster of circulating bat coronaviruses shows potential for human emergence. Nat Med 2015; 21: 1508–13.
- 18 Sallard E, Halloy J, Casane D, van Helden J, Decroly É. Retrouver les origines du SARS-CoV-2 dans les phylogénies de coronavirus. Médecine/Sciences 2020; 36: 783-96.
- 19 Sirotkin K, Sirotkin D. Might SARS-CoV-2 have arisen via serial passage through an animal host or cell culture? A potential explanation for much of the novel coronavirus' distinctive genome. BioEssays 2020; https://dx.doi. org/10.1002%2Fbies.202000091.
- 20 Sari G, van de Garde MDB, van Schoonhoven A, et al. Hepatitis E virus shows more genomic alterations in cell culture than in vivo. Pathogens 2019; 8: 255.
- 21 Daszak, Peter. Understanding the risk of bat coronavirus emergence. NIH grant 5R01Al110964-04. 2014. https://grantome. com/grant/NIH/R01-Al110964-04 (accessed July 13, 2021).
- 22 Hu B, Zeng L-P, Yang X-L, et al. Discovery of a rich gene pool of bat SARS-related coronaviruses provides new insights into the origin of SARS coronavirus. PLoS Pathog 2017; 13: e1006698.
- 23 Schou S, Hansen AK. Marburg and Ebola virus infections in laboratory non-human primates: a literature review. Comp Med 2000; 50:108-23.
- 24 Siengsanan-Lamont J, Blacksell SD. A review of laboratory-acquired infections in the Asia-Pacific: understanding risk and the need for improved biosafety for veterinary and zoonotic diseases. Trop Med Infect Dis 2018; 3: 36.
- 25 Klotz LC, Sylvester EJ. The consequences of a lab escape of a potential pandemic pathogen. Front Public Health 2014; published online Aug 14. https://dx.doi.org/10.3389%2Ffpubh. 2014.00116.

- 26 Heymann DL, Aylward RB, Wolff C. Dangerous pathogens in the laboratory: from smallpox to today's SARS setbacks and tomorrow's poliofree world. Lancet 2004; 363: 1566-68.
- Sewell DL. Laboratory-associated infections and biosafety. Clin Microbiol Rev 1995;
 8: 389-405.
- 28 Zeng L-P, Gao Y-T, Ge X-Y, et al. Bat severe acute respiratory syndrome-like coronavirus WIV1 encodes an extra accessory protein, ORFX, involved in modulation of the host immune response. J Virol 2016; 90: 6573-82.
- 29 Segreto R, Deigin Y, McCairn K, et al. Should we discount the laboratory origin of COVID-19? Environ Chem Lett 2021; 19: 2743–57.
- 30 Piplani S, Singh PK, Winkler DA, Petrovsky N. In silico comparison of SARS-CoV-2 spike protein-ACE2 binding affinities across species and implications for virus origin. Sci Rep 2021; 11: 13063.
- 31 Relman DA. Opinion: To stop the next pandemic, we need to unravel the origins of COVID-19. Proc Natl Acad Sci USA 2020; 117: 29246-48.
- 32 Bloom JD, Chan YA, Baric RS, et al. Investigate the origins of COVID-19. Science 2021; 372: 694.

Authors' reply

We write on behalf of our coauthors1 to agree with Jacques van Helden and colleagues that scientists "need to evaluate all hypotheses on a rational basis, and to weigh their likelihood based on facts and evidence, devoid of speculation concerning possible political impacts". Scientific knowledge is essential to effectively quide future efforts to reduce the chance of another pandemic,1,2 including by mitigating or blocking all relevant pathways for a pathogen to host-shift from natural hosts to humans. Endless arguments back and forth about the emergence of SARS-CoV-2, pitting evolution and spillover in nature against a laboratory leak do little to advance our critical knowledge base. We need more scientific evidence that unravels the likely pathway for the virus because real evidence that confirms or refutes hypotheses is far more important than the hypotheses and conjectures themselves. Expert reviews and new data continue to emerge tracing the evolutionary pathway of SARS-CoV-2 in nature over decades, serving to place some controversial genomic characteristics

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within a broader evolutionary context.3-5 However, while we need more evidence, the world will remain mired in dispute without full engagement of China, including open access to primary data, documents, and relevant stored material to enable a thorough, transparent, and objective search for all relevant evidence. As we have already seen⁶ this engagement is impossible in an environment of implicit or explicit blame placed on the Wuhan Institute of Virology and its scientists. We stand by our statement that "recrimination has not, and will not, encourage international cooperation and collaboration".1

JSM is a member of the WHO International Health Regulations Emergency Committee for COVID-19, a member of the One Health High Level Expert Panel that advises the Food and Agriculture Organization of the UN, the World Organisation for Animal Health, the United Nations Environment Programme, and WHO, and a past member of the scientific advisory committee for the Center for Emerging Infectious Diseases of the Wuhan Institute of Virology (2008-11). JSM has past or ongoing academic and scientific collaborations on coronavirus biology with colleagues in China and several other countries. GTK, SKL, and LS are members of the Lancet Task Force on the Origins and Early Spread of COVID-19 & One Health Solutions to Future Pandemic Threats. MT declares no competing

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- 1 Calisher CH, Carroll D, Colwell R, et al. Science, not speculation, is essential to determine how SARS-CoV-2 reached humans. Lancet 2021; 398: 209-11.
- 2 WHO. WHO Statement on advancing the next series of studies to find the origins of SARS-CoV-2. Aug 12, 2021. https://www.who. int/news/item/12-08-2021-who-statementon-advancing-the-next-series-of-studies-tofind-the-origins-of-sars-cov-2 (accessed Sept 5, 2021).
- 3 Zhou H, Jingkai J, Chen X, et al. Identification of novel bat coronaviruses sheds light on the evolutionary origins of SARS-CoV-2 and related viruses. Cell 2021; 184: 4380-91.

- MacLean OA, Lytras S, Weaver S, et al. Natural selection in the evolution of SARS-CoV-2 in bats created a generalist virus and highly capable human pathogen. PLoS Biol 2021; 19: e3001115.
- Holmes EC, Goldstein SA, Stephen A, et al. The origins of SARS-CoV-2: a critical review. Cell 2021; published online Aug 18. https://doi. org/10.1016/j.cell.2021.08.017.
- 6 Dou E, Rauhala E. China sets back search for covid origins with rejection of WHO investigation proposal. Washington Post July 22, 2021. https://www.washingtonpost. com/world/2021/07/22/china-covid-whowuhan/ (accessed Sept 7, 2021).

Telehealth use in antenatal care? Not without women's voices

Kirsten R Palmer and colleagues¹ assessed integrated telehealth for antenatal care in Australia during the early COVID-19 pandemic. However, the estimated 50% reduction of in-person consultations does not represent the proportion of telehealth consultations received by women. Women included in the intervention gave birth between March 23 and July 26, 2020, which is equivalent to, at most, 4 months of a telehealth-integrated antenatal care schedule. Although not presented, the average duration of antenatal follow-up was probably 2 weeks (implementation period) and 6 weeks (integrated care period), allowing for a maximum of two telehealth visits with three face-to-face consultations. This limited exposure at the end of pregnancy is unlikely to show significant differences in outcomes and we are concerned that the conclusion of no compromise to pregnancy outcomes is premature. We need rigorous studies assessing the implementation of telehealth in comparison with a face-toface model throughout the entire pregnancy.

Furthermore, the investigators' recommendation to adopt telehealth beyond the pandemic fails to consider dimensions of care quality and equity.

Research shows that care quality is compromised by incorporating telehealth into routine maternity care.2,3 High user satisfaction rates with telehealth should be interpreted within the context of the pandemic's restrictive measures and women's intent to reduce the risk of SARS-CoV-2 infection, because qualitative evidence shows that pregnant women who received telephone consultations felt distressed due to scarce faceto-face contact with health-care providers.4 More research is needed on women's perspectives of respectful and quality care during any antenatal care schedule that uses telehealth. Additionally, relying on telehealth can contribute to exacerbating inequalities in maternal health,5 in which financial barriers, technological illiteracy, and mistrust lead to excluding vulnerable women.2

Although Palmer and colleagues show that partial use of telehealth in antenatal care appeared to be a non-inferior alternative to prevent disruption of care during the period of COVID-19 restrictions in the Australian context, unjustified compromises to high-quality, person-centred, and equitable care should not be acceptable as a way forward.

We declare no competing interests.

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- Palmer KR, Tanner M, Davies-Tuck M, et al. Widespread implementation of a low-cost telehealth service in the delivery of antenatal care during the COVID-19 pandemic: an interrupted time-series analysis. Lancet 2021; 398: 41–52.
- 2 Galle A, Semaan A, Huysmans E, et al. A double-edged sword—telemedicine for maternal care during COVID-19: findings from a global mixed-methods study of healthcare providers. BMJ Global Health 2021; 6: e004575.
- Asefa A, Semaan A, Delvaux T, et al. The impact of COVID-19 on the provision of respectful maternity care: findings from a global survey of health workers. medRxiv 2021; published online May 9. https://www.medrxiv.org/ content/10.1101/2021.05.05.21256667v1 (preprint).

